

IN THE CLAIMS

The status of the claims of the present application is listed below:

Claims 1-69: Canceled.

70. (New): An isolated DNA coding for a polypeptide which comprises the amino acid sequence of SEQ ID NO: 1, 2 or 3.

71. (New) The DNA of Claim 70, which codes for a polypeptide comprising the amino acid sequence of SEQ ID NO: 1.

72. (New) The DNA of Claim 70, which codes for a polypeptide comprising the amino acid sequence of SEQ ID NO: 2.

73. (New) The DNA of Claim 70, which codes for a polypeptide comprising the amino acid sequence of SEQ ID NO: 3.

74. (New) A vector comprising the DNA of Claim 70.

75. (New) The vector of Claim 74, which is a plasmid.

76. (New) A plant transformed with the DNA of Claim 70.

77. (New) The plant of Claim 76, which is soybean (*Glycine max*), rapeseed (*Brassica campestris*), cotton (*Gossypium*), sugar beat (*Beta vulgaris*), or sugar cane (*Saccharum officinarum*).

78. (New) The plant of Claim 76, wherein the plant is a dicotyledonous plant.

79. (New) The plant of Claim 78, wherein plant is a *Leguminosae*, *Cruciferae*, *Malvaceae*, *Chenopodiaceae*, or *Gramineae* plant.

80. (New) The plant of Claim 79, wherein the plant is a *Glycine*, *Brassica*, *Gossypium*, *Beta*, or *Saccharum* plant.

81. (New) A plant transformed with the vector of Claim 74.

82. (New) The plant of Claim 81, which is soybean (*Glycine max*), rapeseed (*Brassica campestris*), cotton (*Gossypium*), sugar beat (*Beta vulgaris*), or sugar cane (*Saccharum officinarum*).

83. (New) The plant of Claim 81, wherein the plant is a dicotyledonous plant.

84. (New) The plant of Claim 83, wherein the plant is a *Leguminosae*, *Cruciferae*, *Malvaceae*, *Chenopodiaceae*, or *Gramineae* plant.

85. (New) The plant of Claim 83, wherein the plant is a *Glycine*, *Brassica*, *Gossypium*, *Beta*, or *Saccharum* plant.
86. (New) A host cell transformed with the DNA of Claim 70.
87. (New) The host cell of Claim 86, which is a prokaryotic or a eukaryotic cell.
88. (New) The host cell of Claim 86, which is a bacterial cell.
89. (New) The host cell of Claim 86, which is a plant cell.
90. (New) The host cell of Claim 86, which is a soybean, rapeseed, cotton, sugar beat, or sugar cane cell.
91. (New) A chimeric gene comprising the DNA of Claim 70 operably linked to a transcription regulatory region expressible in plant cells.
92. (New) A plant transformed with the chimeric gene of Claim 91.
93. (New) The plant of Claim 92, which is a soybean, rapeseed, cotton, sugar beat, or sugar cane.

94. (New) A method of modifying the content of raffinose family oligosaccharides in a plant, comprising transforming a plant with the chimeric gene of Claim 91, thereby changing the content of raffinose family oligosaccharides in the plant.

95. (New) The method of Claim 94, wherein the plant is a soybean, rapeseed, cotton, sugar beat, or sugar cane.

96. (New) A method of producing a polypeptide which comprises an amino acid sequence of SEQ ID NO: 1, 2 or 3, comprising culturing the host cell of Claim 90 under conditions where said polypeptide is expressed, and isolating said polypeptide.

97. (New): An isolated DNA molecule encoding a polypeptide having an ability to produce raffinose from sucrose and galactinol, wherein the DNA is hybridizable under stringent conditions to a DNA comprising nucleotide numbers 56 to 2407 of SEQ ID NO: 4, the stringent conditions being 1X SSC, 0.1% SDS at 60°C,

wherein the polypeptide having the ability to produce raffinose from sucrose and galactinol has the following properties:

- (1) optimum pH: the polypeptide has an optimum pH of about 6 to 8;
- (2) optimum temperature: the polypeptide has an optimum temperature of about 35 to 40°C;
- (3) molecular weight: the polypeptide has:
 - (i) a molecular weight of about 75 kDa to 95 kDa estimated by gel filtration chromatography;

(ii) a molecular weight of about 90 kDa to 100 kDa estimated by polyacrylamide gel electrophoresis; and

(iii) a molecular weight of about 90 kDa to 100 kDa estimated by SDS-polyacrylamide gel electrophoresis under a reduced condition; and

(4) inhibition: the polypeptide is inhibited by iodoacetamide, N-ethylmaleimide, and myo-inositol.

98. (New) A vector comprising the DNA of Claim 97.

99. (New) The vector of Claim 98, which is a plasmid.

100. (New) A plant transformed with the DNA of Claim 97.

101. (New) The plant of Claim 100, which is soybean (*Glycine max*), rapeseed (*Brassica campestris*), cotton (*Gossypium*), sugar beat (*Beta vulgaris*), or sugar cane (*Saccharum officinarum*).

102. (New) The plant of Claim 101, wherein the plant is a dicotyledonous plant.

103. (New) The plant of Claim 102, wherein plant is a *Leguminosae*, *Cruciferae*, *Malvaceae*, *Chenopodiaceae*, or *Gramineae* plant.

104. (New) The DNA of Claim 102, wherein the plant is a *Glycine*, *Brassica*, *Gossypium*, *Beta*, or *Saccharum* plant.

105. (New) A plant transformed with the vector of Claim 98.
106. (New) The plant of Claim 105, which is soybean (*Glycine max*), rapeseed (*Brassica campestris*), cotton (*Gossypium*), sugar beat (*Beta vulgaris*), or sugar cane (*Saccharum officinarum*).
107. (New) The plant of Claim 105, wherein the plant is a dicotyledonous plant.
108. (New) The plant of Claim 107, wherein plant is a *Leguminosae*, *Cruciferae*, *Malvaceae*, *Chenopodiaceae*, or *Gramineae* plant.
109. (New) The DNA of Claim 107, wherein the plant is a *Glycine*, *Brassica*, *Gossypium*, *Beta*, or *Saccharum* plant.
- 110 (New) A host cell transformed with the DNA of Claim 97.
111. (New) The host cell of Claim 110, which is a prokaryotic or a eukaryotic cell.
112. (New) The host cell of Claim 110, which is a bacterial cell.
113. (New) The host cell of Claim 110, which is a plant cell.

114. (New) The host cell of Claim 110, which is a soybean, rapeseed, cotton, sugar beat, or sugar cane cell.

115. (New) A chimeric gene comprising the DNA of Claim 97 operably linked to a transcription regulatory region expressible in plant cells.

116. (New) A plant transformed with the chimeric gene of Claim 115.

117. (New) The plant of Claim 116, which is a soybean, rapeseed, cotton, sugar beat, or sugar cane.

118. (New) A method of modifying the content of raffinose family oligosaccharides in a plant, comprising transforming a plant with the chimeric gene of Claim 115, thereby changing the content of raffinose family oligosaccharides in the plant.

119. (New) The method of Claim 118, wherein the plant is a soybean, rapeseed, cotton, sugar beat, or sugar cane.

120. (New) A method of producing a polypeptide comprising culturing the host cell of Claim 110 under conditions where said polypeptide is expressed, and isolating said polypeptide.